

M A S L D R V K V L V L G D S      SEQ ID NO:2  
AGGGAAAGCCAGTGGCAAG ATG CCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA GAC TCA      SEQ ID NO:1  
↑SEQ ID NO:3→

G	V	G	K	S	S	L	V	H	L	L	C	Q	N	Q	V	L	G	N	P	35
GGT	GTT	GGG	AAA	TCT	TCG	TTA	GTC	CAT	CTC	CTA	TGC	CAA	AAT	CAA	GTG	CTG	GGA	AAT	CCA	105
S	W	T	V	G	C	S	V	D	V	R	V	H	D	Y	K	E	G	T	P	55
TCA	TGG	ACT	GTC	GGC	TGC	TCA	GTC	GAT	GTC	AGA	GTT	CAT	GAT	TAC	AAA	GAA	GGA	ACC	CCA	165
E	E	K	T	Y	Y	I	E	L	W	D	V	G	G	S	V	G	S	A	S	75
GAA	GAG	AAG	ACC	TAC	TAC	ACA	GAA	TTA	TGG	GAT	GTT	GGA	GGC	TCT	GTG	GGC	AGT	GCC	AGC	225
S	V	K	S	T	R	A	V	F	Y	N	S	V	N	G	I	I	F	V	H	95
AGC	GTG	AAA	AGC	ACA	AGA	GCA	GTA	TTC	TAC	AAC	TCC	GTA	AAT	GGT	ATT	ATT	TTC	GTA	CAC	285
D	L	T	N	K	K	S	S	Q	N	L	R	R	W	S	L	E	A	L	N	115
GAC	TTA	ACA	AAT	AAG	AAG	TCC	TCC	CAA	AAC	TTG	CGT	CGT	TGG	TCA	TTG	GAA	GCT	CTC	AAC	345
R	D	L	V	P	T	G	V	L	V	T	N	G	D	Y	D	Q	E	Q	F	135
AGG	GAT	TTG	GTG	CCA	ACT	GGA	GTC	TTG	GTG	ACA	AAT	GGG	GAT	TAT	GAT	CAA	GAA	CAG	TTT	405
A	D	N	Q	I	P	L	L	V	I	G	T	K	L	D	Q	I	H	E	T	155
GCT	GAT	AAC	CAA	ATA	CCA	CTG	TTG	GTA	ATA	GGG	ACT	AAA	CTG	GAC	CAG	ATT	CAT	GAA	ACA	465
K	R	H	E	V	L	T	R	T	A	F	L	A	E	D	F	N	P	E	E	175
AAG	CGC	CAT	GAA	GTT	TTA	ACT	AGG	ACT	GCT	TTC	CTG	GCT	GAG	GAT	TTC	ATT	CCA	GAA	GAA	525
I	N	L	D	C	T	N	P	R	Y	L	A	A	G	S	S	N	A	V	K	195
ATT	AAT	TTG	GAC	TGC	ACA	AAT	CCA	CGG	TAC	TTA	GCT	GCA	GGT	TCT	TCC	ATT	GCT	GTC	AAG	585
L	S	R	F	F	D	K	V	I	E	K	R	Y	F	L	R	E	G	N	Q	215
CTC	AGT	AGG	TTT	TTT	GAT	ARG	GTC	ATA	GAG	AAG	AGA	TAC	TTT	TTA	AGA	GAA	GGT	ATT	CAG	645
I	P	G	F	P	D	R	K	R	F	G	A	G	T	L	K	S	L	H	Y	235
ATT	CCA	GGC	TTT	CCT	GAT	CGG	AAA	AGA	TTT	GGG	GCA	GGA	ACA	TTA	AAG	AGC	CTT	CAT	TAT	705
D	*																			237
GAC	TGA																			711
←SEQ ID NO:3↑																				
ATTACACTCATCCTTGGAAAGAGTGAGCAAGCAGTGGCAGTTTTCACAGCTCATCTTGTGTGTTCAATTATTACCAT																				
CACAGCCCTTTAACAAATCATCTTAAATGCTACCCCTCAGCCTTACCTTAAATGGAAAAATGAAAGGAGTGACAA																				
TACGGGAGGTCCAAACTTGTCCCTGTTCTGTGTTCTTACCTTCTGTCCCTGTGTATAGATTATGTAAAGCCTT																				
GTGTAATATGAGATGTTGTCAAATGATGCAAGTAAATGAGCAATGACAGTGTACTGCAGAGAAAATTACTCTTGCCT																				
AGAACTGGAGGGTTTATGGGTCTGTAATTTCACACTCATGCTGAAGCTTAATTAAAGTACTTCATAAACGTAT																				
CTCCATTGTTTACCTTCTTGAGGGAACGGCTTGTAAACCAGCCCTGAGTTGTCTACCCCAACCATCTGTCAATT																				
TTCAAAGATGCAAAATGGGTTATTAAATTGTCTCCACCATGTCACACACAGGAATGCCATAATAAGCARCCCTGT																				
CTCCCTCTCTCCTTGCATAATGGCTAGTGACTGGAAGAGGGCGGACTAATAGCCAGAGTTAAATATAAAACAAAT																				

Title: 47324, A NOVEL HUMAN G-PROTEIN AND USES THEREFOR  
Inventor: Rachel Meyers  
Application No.: To be Assigned  
Docket No.: 381552003500

Sheet 2 of 6

TAATAATACATAGAGAACAGCAATACCAGAAAAAAAGAATTCTGGTAAAATGATGTGAAAAATTGACAGCTCCCTCACT  
CTTAAGGTTGCTATACAGTCTAGGTTCTGTTGGAAATAGGTAGGGTAAATCTAAGACCTGCACAAGGGCA  
GTGAGAGACATTACAGCCTCCTCTATTGTTTTAAGGAAAAGTCAACTCCTGAAATGTCCCTAGCTATAATC  
AGAAAACTAAGAATATTCTGTCAACAATGTATTGAGAGAAGTAAAATAAGTTCCACAGAACACAAAAAA  
CATGAATTATGAACTA

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FIG. 1B

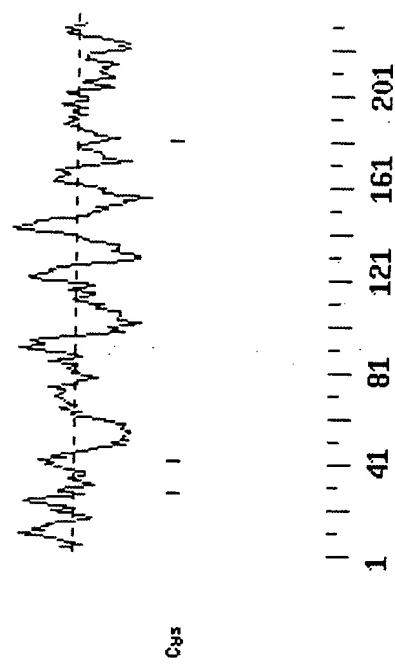


FIG. 2

\*->GlgflkiflkllglwnKEmRILiLGLDnAGKTTILyklklge.ivtt SEQ ID NO:4  
47324 2 -----ASLDR---VKVLVLDGSVGKSSLVHLLCQNQvLGNP 35  
  
iPTiGFNvEtveykN.....ikFtvWDvGGQ.....eslRP1W  
+ T+G v v + +++++++ + WDvGG ++ ++ +s R +  
47324 36 SWTVGCSV-DVRVHDykegtpeektYYIELWDVGGSvgsassvKSTRAV- 83  
  
rnYfpnTdavIfVVDSaDreRieeakeELhaLLneeeL.....  
+ +++++IfV D ++ + + L + e +++ +++ ++  
47324 84 --FYNSVNGIIFVHDLTNKK---SSQNLRRWSLEALNrdlvptgvln 127  
  
.....adApLifANKQD1pgAmseaEi...reaLgLhelkgskg  
++ +++ + plL+ + K D + +E+ +++ L +  
47324 128 gdydqeafadNQIPLLVIGTKLDQIHETKRHEVltrTAFLAEDFNP-E-- 174  
  
kvt1.e.gdRpWeiiggcsAvkGeGLyEGldWLsnnikkkr<-\*  
++ 1+ ++ R + ++Avk l + + +++++  
47324 175 EINLdCtNPRYLAAGSSNAVK-----LSRFFDKVIEK 206

FIG. 3

\*->KLVliGDsGVGKSSlLiRFtdnkFveeYipTIGvDFytktvevD... SEQ ID NO:5  
47324 8 KVLVLDGSVGKSSLVHLLCQNQVGNPSWTVGCSVDVRVHDYKegt 54  
  
.GktvkLqIWDTAGQERFralrpa.....YYRgAqGfLLVYDITs  
++ kt+ ++WD G ++ +a++ +++++ +Y +G++ V D T+  
47324 55 peEKTYIYLWDVGG----SVGSAssvkstravFYNSVNGIIFVHDLTN 99  
  
rdSFenvkkWleelir..had.....kdenvpivLVGNKC  
++S +n+++W e l+++ +++ +++++ +d+ +p + +G+K  
47324 100 KKSSQNLRRWSLEALNrdlVPtgvln 149  
  
DLeddedlelte.gqkRvVsteeGealAkelgA.....1pFmETSA  
D + e++ +V t ++ 1A++++ ++ + + ++ +++ +  
47324 150 DQIH-----EtKR-HEVLTRTAF-LAEDFNPeelinldctnPRYLAAGS 190  
  
KtntNVeeaFeelareilkkvsevnvlldqpakkkskCcil<-\*  
+++ F+ +++++ + +++++++ + +k+ +  
47324 191 SNAVKLRSRFFDKVIEKRYFLREGNQIPGFPD-RKRGAGTLK 231

FIG. 4

Query: 35 PSWTV-GCSVDRVHDYKEGTPEEK--YYIELWDXXXXXXXXXXXXXTRAVFYNSVNGI 91  
P+WT S D + Y TP Y+E +D R FY +++GI  
Sbjct: 69 PTWTPSSSEDSENPYMRSTPTTNILYFVEFYDLNSDWRMCRQQ---RESFYKNIDGI 125 SEQ ID  
NO:6

Query: 92 IFVHDLTNKSSQNLRRWSLEALNRDLVPTGVLVTNGDYDQEKFADNQIPLLVIGTKLDQ 151  
+ V+++ S +L W + L + + + + + P+LV+GT LD+  
Sbjct: 126 VLVYNMELSSQDSLHDWLYDPLRQICKHRHLRI-----RSILKNHNAPILVVGTNLDK 179

Query: 152 IHETKRHEVLTRTAFLAEDFNPEEINLDCTNPRYLAAGSSNAVKSLSRFFDKVIE-KRYF 209  
+ L R +A N EE+ ++C +P+ S N KL F ++VIE K F  
Sbjct: 180 L----MRRPLRRRGSIAHQLNVEEMLVNCLDPQSFVDKSRNQGKLYGFLNRVIEFKEQF 234

FIG. 5a

Query: 7 VKVLVLGDSGVGKSSLVHLLCQNQVLGNP-SWTVG---CSVDVRVHDYKE 52  
V++L+LGD GVGK+SL +L+ ++ P S TVG V VR+H+Y +  
Sbjct: 12 VRILMLGDRGVGKTSLTNLMATTEITPTPDSRTVGEESWHVQVRLHEYSK 61 SEQ ID NO:7

FIG. 5b

Query: 121 TGVLVTNGD--YDQEKFAD-NQIPLLVIGTKLDQIHETKRHEVL--TRTAFLAEDFNPEE 175  
T L T+G +D E+F Q P+LV+GTLD + E KRH + + +A+ EE  
Sbjct: 19 TDNLGTDGHILFDMEFLGATQTPILVMGTKLDLLDE-KRHPKMGVKPGGIADKCGAEE 77 SEQ ID  
NO:8

Query: 176 INLDCTNPRYLAAGSSNAVKSLSRFFDKVIEKRYFLR-----EGNQIPGFDRKRGAG 228  
I L+C N R LAAG+++AVKLSRFFD+VIE R LR + PDR+RFG  
Sbjct: 78 IWLNCRNSRSLAAGTTDAVKLSRFFDRVIENRKALRAALAFGVSSSNAVSPPDRRGPT 137

Query: 229 TLK 231  
+ K  
Sbjct: 138 SAK 140

FIG. 6

Query: 6 RVKVLVLDGSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEGTPEEKTYYIE 63  
+V+VLV+GDSGVGK+SLVHL+ + + P T+GC+V V+ Y G+P + I+  
Sbjct: 80 QVRVLVVGDSGVGKTSLVHLINKSSIVRPPQTIGCTVGVKHITY--GSPASSSSSIQ 135 SEQ ID NO:9

**FIG. 7**

Query: 8 KVLVLGDGSGVGKSSLVHLL--CQNQ-----VLGNPSWTVGCSVDVRVHDYKEGT 54  
K++++GDSGVGK+SL++ L +N V+ + T+G +V+ T  
Sbjct: 7 KIVIIGDSGVGKTSLLNKLRFTENSFTEEYDPTTRTVVDSYKSTIGVDFNVKTIEVVDT 66 SEQ ID  
NO:10

Query: 55 PEEKTYYIELWDXXXXXXXXXXXXXXTRAVFYNSVNGIIFVHDLTNKKSS-QNLRRWSLEA 113  
+ K +++WD A +Y I V+D+ + +SS +N +W E  
Sbjct: 67 -DGKNIKLQIWDTAGQERYRSMLTSMEA-YYRGAEADIIIVYDVDSSESSFENQTKWLKEI 124

Query: 114 LNRDLVPTGVLVTNGDYDQEKFADNQIPLLVIGTKLD-QI---HETKRHEVLRTAFLAE 169  
L +N E+ ++N +P+++G K D ++ E + + T A+  
Sbjct: 125 LRH-----ASN-----EEASEN-VPIILVGNKADLEVNPSEEVEEKEEASTEEEAQ 170

Query: 170 DFNPSEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDRKRF 225  
F EE L P + + + F +++ R L++ +I D+++  
Sbjct: 171 SF-AEEKGLGVV-PFIETSAKTTGTNVEEVFQELV--REILKKKKEIQEKADQEKY 222

**FIG. 8**